



## PreprocessDataset Documentation

**Module name:** PreprocessDataset  
**Description:** Perform several preprocessing options on a res, gct, or Dataset input file  
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**Date:** 04/04/04

**Summary:** The PreprocessDataset module performs a variety of pre-processing operations including thresholding/ceiling, variation filter, discretization and normalization:

Thresholding:

Value = threshold if Value < threshold  
Value = ceiling if Value > ceiling

Variation filter (exclude rows for which):

max / min < minchange  
max – min < mindelta  
here the max and min are computed over a row excluding the top (and bottom) “num.excl” experiments. This is to prevent one or more “spikes” to make the gene pass the filter.

The filter flag controls the application of both thresholding and the variation filter.

Independently of the application of thresholding and the variation filter the module also has a preprocessing flag to turn on the discretization or normalization of the dataset (after thresholding and filtering).

Probability threshold allows sampling of the rows without replacement to obtain that fraction of the total number of rows. The “max sigma binning” parameter controls how many bins are used when discretizing. The default “value of 1” produces binary discretization (above and below the mean).

The module also includes the option to take the log base 2 of all values in the input dataset. Lastly, the module can remove rows in which the given number of columns does not contain a value greater or equal to a user defined threshold.

The order of the steps in the module is as follows:

1. Thresholding
2. Log Base 2
3. Remove row if n columns not >= than given threshold
4. Variation filter

### Parameters:

| Name                | Description                           |
|---------------------|---------------------------------------|
| input.filename:     | input filename - .res, .gct, Dataset  |
| output.file:        | Output file with preprocessed dataset |
| output.file.format: | output file format                    |

# GenePattern

|                    |   |
|--------------------|---|
| filter.flag:       | Variation filter and thresholding flag  |
| preprocessing.flag | Discretization and normalization flag   |
| minchange:         | Minimum fold change for filter  |
| mindelta:          | Minimum delta for filter  |
| threshold:         | Value for threshold   |
| ceiling:           | Value for ceiling   |
| max.sigma.binning: | Maximum sigma for binning   |
| prob.thres:        | Value for uniform probability threshold filter                                |
| num.excl:          | Number of experiments to exclude (max & min) before applying variation filter |
| log.base.two       | Whether to take the log base two after thresholding                           |
| number.of.columns  | Remove row if n columns not $\geq$ than given threshold                       |
| above.threshold    |   |
| column.threshold   | Threshold for removing rows   |

## Return Value:

the filtered, preprocessed output file

## Platform dependencies:

|                        |                    |
|------------------------|--------------------|
| <b>Task type:</b>      | Preprocess&Utility |
| <b>CPU type:</b>       | any                |
| <b>OS:</b>             | any                |
| <b>Java JVM level:</b> | 1.4                |
| <b>Language:</b>       | Java               |